

**In the Specification:**

Please amend the specification as shown:

Please delete the paragraph on page 37, lines 3-5 and replace it with the following paragraph:

Low complexity sequence found by a filter program is substituted using the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNN") (**SEQ ID NO: 1**) and the letter "X" in protein sequences (e.g., "XXXXXXXXXX") (**SEQ ID NO: 2**).

Please delete the paragraph on page 39, lines 6-16 and replace it with the following paragraph:

Fve polypeptides, fragments, homologues, variants and derivatives, are typically made by recombinant means, for example as described below in the Examples. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. The proteins may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis (**SEQ ID NO: 488**), GAL4 (DNA binding and/or transcriptional activation domains) and β-galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences. Preferably the fusion protein will not hinder the function of the protein of interest sequence. Proteins may also be obtained by purification of cell extracts from animal cells.

Please delete the paragraph on page 137, lines 18-26 and replace it with the following paragraph:

The DNA fragment encoding E7 of HPV type 16 is subcloned into pGEX-4T1 protein expression vector. E7 DNA fragment is amplified by polymerase chain reaction (PCR) using a set of primers: 5'-TTGTTGGATCCCATGGAGATAACACCTACATTG-3' (**SEQ ID NO: 3**) and 5'- TTACTGAATTCTATGGTTCTGAGAACAGATG-3' (**SEQ ID NO: 4**). The amplified DNA is digested with BamH1 and EcoR1, and the resulting fragment is then cloned into the BamH1 and EcoR1 sites of pGEX- 4T1 vector. The presence of the inserted E7 is confirmed by restriction enzyme digestion and gel electrophoresis. The accuracy of the constructs is further confirmed by DNA sequencing. The plasmid construct is transformed into Escherichia coli TG-1 for protein expression.

Please delete Appendix A on pages 160-171, and replace it with the following Appendix:

#### Appendix A: Sequences

Fve is isolated from Golden Needle Mushroom (*Flammulina velutipes*). ORGANISM: Flammulina velutipes. Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales; Tricholomataceae; Flammulina.

##### *Fve (Wild type)*

ATGTCCGCCACGTCGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCC  
CAACTGGGGCCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCAGACA  
AAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGAGTGACA  
CCGTCGGTGGGAGACCATCAACTTCCCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAAC  
GATTCAAGTTTCGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAAGA  
AGACTTGA (**SEQ ID NO: 5**)  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvldkksyrvvvngsdlgvesnfavt  
psggqtinflynkgygvadktiqvfvipdtgnseeyiaewkkt (**SEQ ID NO: 6**)  
ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA (**SEQ ID NO: 5**)

A Fve (Wild type) sequence may also comprise a sequence as set out above, but lacking the initial methionine (M) in the amino acid sequence, or lacking the initial ATG in the nucleic acid sequence.

*GST-Fve (Wild type) Nucleotide Sequence*

ATGTCCCCATACTAGTTATTGGAAAATTAAGGCCTTGTGCAACCCACTGACTTCTTT  
GGAATATCTGAAGAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAATGGC  
GAAACAAAAAGTTGAATTGGGTTGGAGTTCCCAATCTTCCTTATTATATTGATGGTGT  
GTTAAATTAACACAGTCTATGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGG  
TGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTGAAGGAGCGGTTGGATATTAGAT  
ACGGTGTTCGAGAATTGCATATAGTAAAGACTTGAACACTCTCAAAGTTGATTTCTTAGC  
AAGCTACCTGAAATGCTGAAAATGTCGAAGATCGTTATGTCATAAAACATATTAAATGG  
TGATCATGTAACCCATCTGACTTCATGTTGTATGACGCTCTGATGTTGTTATACATGG  
ACCCAATGTGCCTGGATGCGTCCAAAATTAGTTGTTAAAAACGTATTGAAGCTATC  
CCACAAATTGATAAGTACTGAAATCCAGCAAGTATATAGCATGGCCTTGAGGGCTGGCA  
AGCCACGTTGGTGGTGGCGACCACCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGC  
CCCTGGGATCCTCCGCCACGTCGCTCACCTCCAGCTGCCTACTTGGTGAAGAAGATCGAC  
TTCGACTACACCCCCAACCTGGGGCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTT  
CCCCAAGGTTCTCACCGACAAAAAAATCTGTAACCGCGTCGGTCAATGGCTCTGACCTTG  
GCGTCGAGTCCAACCTCGCAGTGACACCCTCCGGTGGCAGACCATCAACTCCTCCAGTAC  
AACAAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTCTGTTGCAATTCCAGATAC  
CGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAAGAAGACTTGA **(SEQ ID NO: 7)**

*GST-Fve (Wild type) Amino Acid Sequence*

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHYERDEGDKWRNKKFELGLEFPNLPYIYGDVKLTQS  
MAIIRYIADKHNMLGGCPKERAEISMLEGAVIDIRYGVSRIAYSKDFETLKVDLSPKLEMKFEDR  
LCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOQIDKYLKSSKYIAWPLQ  
GWQATFGGGDHPPKSDELVLFQGPLGSSATSLTFQLAYLVKKIDFDYTPNWGRGTPSSYIDNLTFPKV  
LTDKKYSYRVVVNGSDLGVESNFAVTPSGGQTINFLQYNKGYGVADTKTIQVFVVIPTGNSEYIIA  
EWKKT **(SEQ ID NO: 8)**

**FVE DELETION MUTANTS**

*Fve D6-18*

ATG/TCC/GCC/ACG/TCG/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/  
AGC/AGC/TAC/ATC/GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/  
TAC/TCG/TAC/CGC/GTC/GTG/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/  
TTC/GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/  
AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/  
CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/  
TGA **(SEQ ID NO: 9)**

msats/fdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavtpsggqtinflqy  
nkgygvadtktiqvfvvipdtgnseeyiiawekkt **(SEQ ID NO: 10)**

Fve D19-33

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/ATC/GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/  
TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/  
GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/  
TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/  
ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ  
ID NO: 11)**

msatsltfqlaylvkkid/idnltfpkvltdkksyrvvvngsdlgvesnfavtpsggqtinflqynk  
gygavadktiqvfvvipdtgnseeyiliaewkkt **(SEQ ID NO: 12)**

Fve D34-46

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/AAA/  
TAC/TCG/TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/  
TTC/GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/  
AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/  
CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/  
TGA **(SEQ ID NO: 13)**

msatsltfqlaylvkkidfdytpnwgrgtpssy/kysyrvvvngsdlgvesnfavtpsggqtinflqy  
nkgygavadktiqvfvvipdtgnseeyiliaewkkt **(SEQ ID NO: 14)**

Fve D47-60

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/GTC/GAG/TCC/AAC/TTC/  
GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/  
GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/  
GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA  
**(SEQ ID NO: 15)**

msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdk/vesnfavtpsggqtinflqyn  
kggygavadktiqvfvvipdtgnseeyiliaewkkt **(SEQ ID NO: 16)**

Fve D61-72

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/  
AAC/AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/  
ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/  
ACT/TGA **(SEQ ID NO: 17)**

msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkksyrvvvngsdlg/qtinflq  
ynkggygavadktiqvfvvipdtgnseeyiliaewkkt **(SEQ ID NO: 18)**

Fve D73-84

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/

ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/  
ACT/TGA (SEQ ID NO: 19)  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkksyrvvvngsdlgvesnfavt  
psgg/gvadtktiqvfvvipdtgnseeyiliaewkkt (SEQ ID NO: 20)

Fve D85-97

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GTC/  
ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/  
ACT/TGA (SEQ ID NO: 21)  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkksyrvvvngsdlgvesnfavt  
psggqtinflqynkgy/ipdtgnseeyiliaewkkt (SEQ ID NO: 22)

Fve D98-106

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/TAC/ATC/ATC/GCT/GAG/  
TGG/AAG/AAG/ACT/TGA (SEQ ID NO: 23)  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkksyrvvvngsdlgvesnfavt  
psggqtinflqynkgyvadtktiqvfvv/yiaeawkkt (SEQ ID NO: 24)

Fve D107-115

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TGA (SEQ ID NO: 25)  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkksyrvvvngsdlgvesnfavt  
psggqtinflqynkgyvadtktiqvfvvipdtgnsee/ (SEQ ID NO: 26)

Fve D61-97

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/  
GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA (SEQ ID NO: 27)  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkksyrvvvngsdlg/ipdtgns  
eeyiliaewkkt (SEQ ID NO: 28)

*Fve p55-100*

AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/CCG/TCC/GGT/  
GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/GTC/GCG/GAC/  
ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ **(SEQ ID NO: 29)**  
Ngsdlgvesnfavtpsgqqtinflqynkgygadtktiqvfvvipd **(SEQ ID NO: 30)**

**FVE MUTANTS WITH SINGLE AMINO ACID SUBSTITUTIONS**

*FveR27A*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/GCA/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 31)**  
msatsltfqlaylvkkidfdytpnwga~~gt~~pssyidnltfpkvldkkysrvvvngsdlgvesnfavt  
psggqtinflqynkgygadtktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 32)**

*FveG28A*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GCA/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 33)**  
msatsltfqlaylvkkidfdytpnwgrat~~p~~pssyidnltfpkvldkkysrvvvngsdlgvesnfavt  
psggqtinflqynkgygadtktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 34)**

*FveT29A*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/GCA/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 35)**  
msatsltfqlaylvkkidfdytpnwgrgapssyidnltfpkvldkkysrvvvngsdlgvesnfavt  
psggqtinflqynkgygadtktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 36)**

## FUSION PROTEINS OF MAJOR HOUSE DUST MITE ALLERGEN (BL0 T 5 OR DER P 2) AND FUNGAL IMMUNOMODULATORY PROTEIN FVE

### *Blo t 5-Fve (two-in-one chimeric wild type)*

caagagcacaaggccaaagaaggatgattccgaaacgaattcgatcaacttgcatacgaaacaggcaaa  
ccatgttatcgaaaagggagaacatcaattgtttacttgcaacaccactcgacgaaatgtaaaa  
acaagagcaaggaaattcaagagaaaaatcattcgagaactgtatgtttgcgccatgtcgaaggaa  
gcccaggagcttggAACGTGAATTGAAGCGAACTGATCTTAACATTGGAAACGATTCAACTACGAA  
AGAGGCTCAAACCTCTAGCAAGATCTTGCTTAAGGATTGAAGGAAACCGAACAAAAAGTGAAGGATA  
TTCAAACCCAACTCCGCCACGTCGCTCACCTCCAGCTTGCTACTGGTGAAGAAGATCGACTTCGAC  
TACACCCCCAACTGGGGCCGTGGTACCCAAAGCAGCTACATCGACAACCTTACCTCCCCAAGGTTCT  
CACCGACAAAAAAATCTCGTACCGCGTGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTCG  
CAGTGACACCGTCCGGTGGCAGACCATCAACTCCCTCCAGTACAACAAGGGGTATGGTGTGCGGGAC  
ACCAAAACGATTCAAGTTTGTGTCATTCCAGATACCAGCAACTCGGGAGGAGTACATCATCGCTGA  
GTGGAAGAAGACTG**(SEQ ID NO: 37)**  
QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQLDELNENKSKELEQEKIIRELDVVCAMIEG  
AQGALERELKRTDNLILERFNYEEAQLSKILLKDLKETEIQVKVDIQTQsatsltfqlaylvkkidfd  
ytpnwgrgtpssyidnltpkvldkksyrvvvvngsdgvesnfavtpsggqtinflqynkgygvad  
tktiqfvvvpdtgnseeyiaewkkt **(SEQ ID NO: 38)**

### Blot 5-FveR27A (two-in-one chimeric mutant)

caagagcacaagccaaagaaggatgattccgaaacgaattcgatcacttggatcgAACAGGCAA  
ccatgttatcgaaaaggagaacatcaattgtttacttgcaacaccaactcgacgaattgaatgaaa  
acaagagcaaggaatttgcagagaaaaatcatcgagaacttgcattttttggaaacgatccaactacga  
gcccaaggagcttggaaacgtgaatttgcggaaactgatcttgcattttggaaacgatccaactacga  
agaggctcaaacttcagcaagatcttgcggaaacttgcggaaacgatccaactacga  
ttcaaacccaaTCCGCCACGTCGTCACCTCAGCTTGCGTACTTGGTGAAGAAGATCGACTTCGAC  
TACACCCCCAACTGGGGC**GCA**GGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTT  
TCACCGACAAAAAAACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTC  
GCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCCTCAGTACAACAAAGGGGTATGGTGTGCGGGA  
CACCAAAACGATTCAAGTTTGTGTCATTCCAGATAACCGGCAACTCGGAGGAGTACATCATCGCTG  
AGTGGAAAGAAGACTTGA (**SEQ ID NO: 39**)  
QEHPKPKDDFRNEFDHLLIEQANHAIKEGHEHQLLYLHQQLDELNENKSKELEQEKIIRELDVVVCAMIEG  
AQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKETEQKVKDIQTQsatsltfqlaylvkkidfd  
ytpnwga~~gtpssyidnltpfvldkksyrvvvngsdgvesnfavtpsggqtinflqy~~nkgygvad  
tktiqvfvvipdtqnseeyiaewkkt (**SEQ ID NO: 40**)

#### *Blo t 5-FveT29A (two-in-one chimeric mutant)*

caagagcacaaggccaaagaaggatgattccgaaacgaattcgatcacttgcgttatcgaaacaggcaa  
ccatgctatcgaaaagggagaacatcaattgtttacttgcaacaccactcgacgaattgaatgaaa  
acaagagcaaggaaattgcagagaaaaatcattcgagaactgtatgtttgcgccatgtcgaggaa  
gcccaggagcttggAACGTCATTGGAAACGATTCAGTACAGA  
agaggctcaaactctcagcaagatcttgcttaaggatttgaaaggaaaccgaacaaaaagtgaaggata  
ttcaaaacccaaTCCGCCACGTCGCTCACCTCAGCTTGCTACTGGTGAAGAAGATCGACTTCGAC  
TACACCCCCAACTGGGGCCGTGGT**GCA**CCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTT  
TCACCGACAAAAATACTCGTACCGCGTCGTGGCAATGGCTCTGACCTTGGCGTCGAGTCCAAC  
GCAGTGACACCGTCCGGTGGCAGACCATCAACTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGA  
CACCAAAACGATTCAAGTTCGTTGTCACTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTG  
AGTGGAAAGAAGACTTGA (**SEQ ID NO: 41**)

QEHKPKKKDDFRNEFDHLLIEQANHAIEKGEHQQLYLQHQQLDELNENKSKELEQEKKIRELDVVVCAMIEG  
AQGALERELKRTDNLNILERFNYEEAQTLSKILLKDLKETEQKVKDIQTQsatsltfqlaylvkkidfd  
ytpnwrga~~pssyidnltfpkvltdkkysrvvvngsdlgvesnfavtpsgqqtinflqynkgygvad~~  
~~tktiqvfvvipdtgnseeyiaewkkt~~ (**SEQ ID NO: 42**)

*Der p 2-FveR27A (two-in-one chimeric mutant)*

gatcaagtgcgtcaaagattgtccaatcatgaaatcaaaaaagtttggtaccaggatgccatgg  
ttcagaaccatgtatcattcatcgtaaaaccattccaatttggaaagccgtttcgaagccaaccaaa  
acacaaaaacggctaaaattgaaatcaaaggcctcaatcgatggtttagaagtttatgttcccggtatc  
gatccaaatgcattacatgaaatgcccattggtaaaaggacaacaatatgatattaaatatac  
atgaaatgttccaaaattgcaccaaaatctgaaaatgttgcgtcactgtttaaagttatgggtatg  
atggtgtttggcgtgtcattgctactcatgctaaaatccgcattTCCGCCACGTCGCTCACCTC  
CAGCTTGCTACTTGGTGAAGAAGATCGACTACACCCCCAACTGGGGC**GCA**GGTACCCCAA  
GCAGCTACATCGACAACCTTACCTTCCCAAGGTTCTCACCGACAAAAAAACTCGTACCGCGTCGTG  
GTCATGGCTCTGACCTTGGCGTCGAGTCCAACCTCGCAGTGCACACCGTCCGGGGCAGACCATAA  
CTTCCTCCAGTACAACAAGGGTATGGTGTGCGGACACCAAAACGATTCAAGTTTGTGTTGATT  
CAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAAGAAGACTTGA (**SEQ ID NO: 43**)  
DQDVVKDCANHEIKVLVPGCHGSEPCIIRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGI  
DPNACHYMKCPLVKGQQYDIKYTNVPKIAPKSENVVTVKVMGDDGVLACAIATHAKIRDsatltf  
qlaylvkkidfdytpnwrga~~gtpssyidnltfpkvltdkkysrvvvngsdlgvesnfavtpsgqqtin~~  
~~flqynkgygvadtktiqvfvvipdtgnseeyiaewkkt~~ (**SEQ ID NO: 44**)

*Der p 2-FveT29A (two-in-one chimeric mutant)*

gatcaagtgcgtcaaagattgtccaatcatgaaatcaaaaaagtttggtaccaggatgccatgg  
ttcagaaccatgtatcattcatcgtaaaaccattccaatttggaaagccgtttcgaagccaaccaaa  
acacaaaaacggctaaaattgaaatcaaaggcctcaatcgatggtttagaagtttatgttcccggtatc  
gatccaaatgcattacatgaaatgcccattggtaaaaggacaacaatatgatattaaatatac  
atgaaatgttccaaaattgcaccaaaatctgaaaatgttgcgtcactgtttaaagttatgggtatg  
atggtgtttggcgtgtcattgctactcatgctaaaatccgcattTCCGCCACGTCGCTCACCTC  
CAGCTTGCTACTTGGTGAAGAAGATCGACTACACCCCCAACTGGGGCGTGGT**GCA**CCAA  
GCAGCTACATCGACAACCTTACCTTCCCAAGGTTCTCACCGACAAAAAAACTCGTACCGCGTCGTG  
GTCATGGCTCTGACCTTGGCGTCGAGTCCAACCTCGCAGTGCACACCGTCCGGGGCAGACCATAA  
CTTCCTCCAGTACAACAAGGGTATGGTGTGCGGACACCAAAACGATTCAAGTTTGTGTTGATT  
CAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAAGAAGACTTGA (**SEQ ID NO: 45**)  
DQDVVKDCANHEIKVLVPGCHGSEPCIIRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGI  
DPNACHYMKCPLVKGQQYDIKYTNVPKIAPKSENVVTVKVMGDDGVLACAIATHAKIRDsatltf  
qlaylvkkidfdytpnwrga~~apssyidnltfpkvltdkkysrvvvngsdlgvesnfavtpsgqqtin~~  
~~flqynkgygvadtktiqvfvvipdtgnseeyiaewkkt~~ (**SEQ ID NO: 46**)

*Blot 5-Der p 2-FveR27A (three-in-one chimeric mutant)*

caagagcacaagccaaagaaggatgttccgaaacgaattcgatcactgttgcatacgaaacaggcaaa  
ccatgtatcgaaaaggagaacatcaattgttacttgcaccaactcgacgaaattgaatgaaa  
acaagagcaaggaaattgcaagagaaaatcattcgagaacttgcatttgcgttgcgcattgatcgaaagg  
gccccaggagcttggAACGTGAATTGAGCGAACTGATCTTAACATTTGGAAACGATTCAACTACGA  
AGAGGCTAAACTCTCAGCAAGATCTTGCCTAAGGATTGAGGAAACCGAACAAAAGTGAAGGATA  
ttcaaaaccaagatcaagtgcgtcaaagattgtccaatcatgaaatcaaaaaagtttggtacca  
ggatgccatggtcagaaccatgtatcattcatcgtaaaaccattccaatttggaaagccgtttcga  
agccaaacaaaacacaaaacggctaaaattgaaatcaaaggcctcaatcgatgtttagaagttgatg  
ttcccggtatcgatccaaatgcattacatgaaatgcccattggtaaaaggacaacaatatgat  
attaaatatacatgaaatgttccgaaatgcaccaaaatctgaaaatgttgcgtcactgtttaaagt

tatgggtatgtatgggtttggcctgtgctattgctactcatgctaaaatccgcgatTCCGCCACGT  
CGCTCACCTCCAGCTTGCTACTTGGTGAAGAAAGATCGACTTCGACTACACCCCCA**ACTGGGC**  
**GC**  
**A**GGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCGACAAAAAAACTCGT  
ACCGCGTCTGGTCAATGGCTCTGACCTTGGCGTCAGTCCA**ACTTCG**CAGTGACACC**GTCCGGT**GGG  
CAGACCATCAACTCCTCCAGTACAACAAGGGGTATGGT**TCG**CGGACACCAAAACGATTCAAGTTT  
CGTGTCAATTCCAGATA**CCGG**CACTCGGAGGAGTACATCATCGCTGAGTGGAAAGAAGACTTGA  
**(SEQ ID NO: 47)**  
QEHPKKDDFRNEFDHLLIEQANHAIKGEHQQLLYLQHQQLDELNENKS**KELQE**KIIRELDVVVCAMIEG  
AQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKETEQKV**KD**IQTQDQVDVKDCANHEIKVLVP  
GCHGSEPCIIRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQQYD  
IKYTWNVPKIAPKSENVVVTVKVMDDGVLACAIATHAKIRD**satsltfq**laylvkkidfdytpnwg**a**  
gtpssyidnlfpkvltdkksyrvvvngsdlgvesnfavt**psggqtinflqynkgyg**vadtktiqvfv  
vviptgnseeyiaewkkt **(SEQ ID NO: 48)**

#### FUSION PROTEINS OF VIRAL ANTIGEN AND FVE

##### HPV E7-FveT29A

MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEDEIDGPAGQAEPDRAHYNIVTFCCCDSTLR  
VQSTHVDIRTLLEDLLMGTILGIVCPICSQKPsatsltfq**laylvkkidfdytpnwg**rgapssyidnl  
fpkvltdkksyrvvvngsdlgvesnfavt**psggqtinflqynkgyg**vadtktiqvfv  
vviptgnseeyiaewkkt **(SEQ ID NO: 49)**  
atgcatggagatacacctacattgcatgaatatatgttagatttgcaccaggacaactgatctcta  
ctgttatgagcaattaaatgacagctcagaggaggaggatgaaatagatggtcagctggacaaggcag  
aaccggacagagccccattacaatattgtaaccttttgtcaagtgtgactctacgcttcgggtgtc  
gtacaaaggcacacacgttagacattcgtaactttggaaagacactgttaatggcacacttaggaattgtgt  
ccccatctgttcagaaaccaTCGCCACGTCGTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGA  
TCGACTTCGACTACACCCCCA**ACTGGGCCG**TGGTGCACCAAGCAGCTACATCGACAA**CC**TTACCTTC  
CCCAAGGTTCTCACCGACAAAAAA**ACTCGTACCGCGT**CGTGGTCAATGGCT**CTGAC**CTTGGCGTCGA  
GTCCA**ACTTCG**CAGTGACACCGTCCGGTGGGAGACCATCAACTCTCCAGTACAACAAGGGTATG  
GTGTCGGACACCAAAACGATTCAAGTTT**CGT**TGTCATTCCAGATA**CCGG**CACTCGGAGGAGTAC  
ATCATCGCTGAGTGGAAAGAAGACTTGA **(SEQ ID NO: 50)**

##### HCV Core23-FveT29A

Deletion of the 23 amino acids of core antigen from 141-163 amino acid residues  
leads to increased protein production efficiency

MSTNPKPQRKT**RNTNRRPQDVKFPGGGQIVGGVYLLPRRG**PRLGVRA**TRKT**SERSQPRGRQPIPKA  
RQPEGRAWAQPGYPWPLYGNEGLWAGWLSPRGSRPSWGPTDPRRSRN**LGV**IDTLTCGFADLMGY  
LPLVYATGNLPGCSFSIFLALLSCLTIPASA**satsltfq**laylvkkidfdytpnwg**rgapssyidnl**  
tfpkvltdkksyrvvvngsdlgvesnfavt**psggqtinflqynkgyg**vadtktiqvfv  
vviptgnseeyiaewkkt **(SEQ ID NO: 51)**  
atgagcacgaatcctaaacctaagaaaaaccaa**acgt**aacccaaccgcccacaggacgtcaa  
gttcccccggcgggtggtcagatcgtcggtggagttacctgttgcgcgcaggggccccaggttgggt  
tgcgcgcgacttaggaagacttccgagcggtcgcaacctcgta**ggaa**ggcgcacaacctatccccaggt  
cgccagccccgagggttagggctggctcagccccggtagccctggccctatggcaatgaggc  
gggtggcaggatggctcctgtcaccctgtggctcggcctagttgggccccacggaccccg

gtaggtcgcaattggtaaggcatcgataccctcacgtcgccgttcgcgatctcatgggtac  
cttccgctcgccgcaacaggaaatctgcccgttgctcctttctatcttccttggcttgc  
gtcctgttgcacatcccagcttcgcattgaagTCCGCCACGTGCTCACCTTCCAGCTTGCCTAC  
TTGGTGAAGAAGATCGACTTCGACTACACCCCCAACTGGGGCGTGGTGCACCAAGCAGCTACATCGA  
CAACCTTACCTCCCCAAGGTTCTCACCGACAAAAAAACTCGTACCGCGTGTGGTCAATGGCTCTG  
ACCTGGCGTCGAGTCAACTCGCAGTGACACCGTCCGGTGGCAGACCATAACTCCTCCAGTAC  
AACAAAGGGTATGGTGTGCGGACACCAAAAGATTCAAGTTCTGATCCAGATACCGGCAA  
CTCGGAGGAGTACATCGCTGAGTGGAAAGACTTGA **(SEQ ID NO: 52)**

#### FUSION PROTEINS OF TUMOR-ASSOCIATED ANTIGEN AND FVE

##### MAGE3-FveT29A

mplesqrshckpeegleargealglvgaqapateeqeaasssstlvevtlgevpaaespdpqqspqga  
sslpttmnyplwsqsyedssnqeeegpstfpdlesefqaalsrkvaelfhllkyrarepvtkaeml  
gsvvgnwqyffpvifskassslqlvfielmevdipighlyifatclgsydgllgdqnqimpkagllii  
vlaiiaregdcapeekiweelsvlevfegredsilgdpklltqhfvqenyleyrqvpgsdpacyefl  
wgpralvetsvkvhlhmvkisggphisypplhewvlregeesatsltfqlaylvkkidfdytpnwgr  
gapssyidnltpkvltdkksyrvvvngsdlgvesnfavtpsggqtinflqynkgygvadtktiqv  
vvipdtgnseeyiiaewkkt **(SEQ ID NO: 53)**

atgcctctttagcaggaggactcagactgcaaggcctgaagaaggccttgaggcccggaggaggccc  
gggcctgggtgggtgcgcaggctctgctactgaggaggcaggctgcctcctcttactctag  
ttgaagtccacctggggagggtgcctgctgccagtcaccagatcccccagactcctcaggagcc  
tccagcctccccactaccatgaactaccctctggagccaatcctatgaggactccagcaaccaaga  
agaggaggggccaagcacccctgacctggagtccagttcaagcagcactcagtaggaaggtag  
ccgagttggtcatttctgtcctcaagtatcgagccaggagccgtcacaaaggcagaaatgctg  
gggagtgtcgtcgaaattggcagtattcttcctgtatctcagcaagcttcagttccagttc  
gctggctttggcatcgagctgatggaaagtggacccatggccacttgtacatcttgcaccc  
tgggcctctcatacgatggctgtgggtgacaatcagatcatgccaaggcaggccctctgataatc  
gtcctggccataatcgcaagagaggcgactgtgcccctgaggagaaaatctgggaggagctgag  
gttagaggtttgaggggaggaaagacagtatctggggatccaaagaagctgctcaccaacatt  
tcgtcaggaaaactaccctggagttaccggcaggtcccgccagtgatcctgcatgttatgaatt  
tggggtccaaggccctcggtgaaaccagctatgtgaaagtctgcaccatatgtaaagatcag  
aggacccatccatccatccaccaccctgcattgagtttgagagaggggaaagagTCGCCACGT  
CGCTCACCTCCAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCCAACTGGGGCGT  
GGTCACCAAGCAGCTACATCGACAACCTTACCTCCCCAAGGTTCTCACCGACAAAAAAACTCGTA  
CCGCGTGTGGTCAATGGCTCTGACCTTGGCGTGCAGTCCAACCTCGCAGTGACACCGTCCGGTGGC  
AGACCATCAACTCCTCCAGTACAACAAGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTC  
GTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCGCTGAGTGGAAAGAAGACTTGA **(SEQ  
ID NO: 54)**

##### MART1-FveT29A

mpredahfiygpkkghghsytttaaaaagigiltvilgvllligcwycrrrnrgyralmdkslhvgtqc  
altrrcpqegfdhrdskvslqekncepvpvnappayeklsaeqsppyspsatsltfqlaylvkkid  
dytpnwrgapssyidnltpkvltdkksyrvvvngsdlgvesnfavtpsggqtinflqynkgyva  
dtktiqvfvipdtgnseeyiiaewkkt **(SEQ ID NO: 55)**

atgccaagagaagatgctacttcatctatggtaaaaaagaaggggcacggccactcttacaccac  
ggctgaagaggccgctggatcgcatcctgacagtgtatctggagtcttactgctcatcgcttt  
ggtagttgtagaagacgaaatggatacagagccttgcggataaaagtcttcatgttggcactcaatgt  
gccttaacaagaagatgcccacaagaagggttgcattcgggacagcaaagtgtcttcaagagaa  
aaactgtgaacctgtggttccaatgctccacccgcattgagaaactctctgcagaacagtcaccac

caccttattcacctTCCGCCACGTCGCTCACCTCCAGCTTGCTACTTGGTGAAGAAGATCGACTTC  
GACTACACCCCCAACTGGGGCGTGGTCACCAAGCAGCTACATCGACAACCTAACCTCCCAAGGGT  
TCTCACCGACAAAAAAACTCGTACCGCGTGTGGTCAATGGCTCTGACCTTGGCGTGCAGTCCAACCT  
TCGCAGTGACACCGTCCGGTGGGAGACCATCAACTTCCTCCAGTACAACAAGGGTATGGTGTCCGG  
GACACCAAAACGATTCAAGTTTCGTTGTCAATTCCAGATAACCGGCAACTCGGAGGAGTACATCATCGC  
**TGAGTGGAAAGAAGACTTGA (SEQ ID NO: 56)**

CEA-FveT29A

kltiestpfnvaegkevlllvhnlpqhlfgywykgervdgnrqiigvyigtqqtppgpaysgreiyy  
pnaslligniiqnndtgfylhvksdlvneeatggfrvypelpkpsissnnskpvedkdavaftcepe  
tqdatylwwvnqslpvspqrqlsngrtltlfnvtrndtasykcetqnpvsarrsdsvilnvygpd  
aptisplntsyrsgenlnlschaasnppaqyswfvmgtfqgstqelfipnitzvnnsgsyticahnsdt  
glnrttvttitvyaeppkpfitssnsnpvededavalteccepeiqnttylwvvnqslpvspqrqlsnd  
nrtlt1svtrndvgpyecginqelsvdhsdpvilnvlygpddptispsytyyrgpvnl1schaasn  
ppaqyswlidgninghtqelfisniteknsglytcqannsasghsrttvktitvsaelpkpsissnns  
kpvedkdavaftcepeaqnttylwvvnqslpvspqrqlsngnrtltlfnvtrndarayvcgiqnsvs  
anrsdpvtldvlygpdtspiisppdssylsganlnlschsasnpspqywsringipqghtqvlfiakit  
pnnngtyacfvsnlatgrnnsvksitvsasgtspglsagatvgimigvlvgvalisatsltfqlayl  
vkkidfdytpnwrgapssyidnltpkvltdkkysyrvvvngsdgvesnfavtpsggqtinflqyn  
kgygvadtktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 57)**  
aagctcaattgaatccacccgttaatgtcgagggggaaaggagggtgctctacttgtccacaa  
tctgcccagcattttgctacagctggataaaaggtgaaagagtggatgcaaccgtcaaatta  
taggatatgtaataggaactcaacaagctaccccgaggccgcatacagtggcgagagataatatac  
ccaaatgcattccgtctgatccagaacatcatccagaatgacacaggattcacccctacacgtcat  
aaagtcaagatcttgtgaatgaagaagaactggccagttccgggtataccggagctgccaagccct  
ccatctccagcaacaactccaaacctggaggacaaggatgtgtggcctcacctgtgaacctgag  
actcagagcgaacctacctgtggtaaacaatcagagcctcccggtcagtcggcaggctgcagct  
gtccaatggcaacaggaccctactctattcaatgtcacaagaaatgacacagcaagctacaatgt  
aaacccagaaccaggactgtagtgccaggcgcagtcattcgtcatcctgaatgtcctcatggccggat  
gccccaccattccctctaaacacatcttacagatcagggaaaatctgaacctctcctgcatgc  
agcctctaaccacactgcacagtactcttggtgtcaatggacttccagcaatccacccaagagc  
tcttatcccaacatcactgtgaataatagtggatcctatacgtgccaagccataactcagacact  
ggcctcaataggaccacagtcaagcagatcacagtctatgcagagccacccctcatcaccag  
caacaactccaaacctggaggatgaggatgtgttagcctaacctgtgaacctgagattcagaaca  
caacctacactgtggtaaataatcagagcctcccggtcagtcggcaggctgcagctgtccaaatgac  
aacaggaccctactctactcagtgtcacaaggaatgttaggaccctatgagtgtggatccagaa  
cgaattaagtgtgaccacagcgcaccaggatcattcgtgaatgtcctcatggccagacgacccca  
tttccctcatacacctattaccgtccagggtgaacctcagccttcctgcattcagcctctaa  
ccacctgcacagtattcttgctgatggaaacatccagcaacacacacaagagctttatctc  
caacatcactgagaagaacagcggactctatacctgcagggcaataactcagccagtgccacagca  
ggactacagtcaagacaatcacagtctgcggagctgccaagccctccatctccagcaacaactcc  
aaacctggaggacaaggatgtgtggcctcacctgtgaacctgaggctcagaacacaacctac  
gtggtggttaatggtcagagcctccaggatcagtcggcactcgactgtccatggcaacaggaccc  
tcactctattcaatgtcacaagaaatgacgcaagagcctatgtatgtggatccagaactcagttagt  
gcaaccgcagtcaccaggatcaccctggatgtcctctatggccggacaccccatcattcccccc  
agactcgtcttaccttcggagcgaacctcaacctctcctgcactcggccttaaccatccccgc  
agtattcttggcgatcaatggataccgcagcaacacacacaagttctttatgcggaaaatcagc  
ccaaataataacgggacctatgcctgtttgtctactggctactggccgcaataattccatagt  
caagagcatcacagtctctgcattcgaacttccctggctctcagctggggccactgtcgccatca  
tgattggagtgtctggttgggttgctgtataTCGCCACGTCGCTCACCTTCAGCTTGCTACTTG  
GTGAAGAAGATCGACTTCGACTACACCCCCAACCTGGGGCGTGGTGCACCAAGCAGCTACATCGACAA

CCTTACCTCCCCAAGGTTCTCACCGACAAAAAAACTCGTACCGCGTCGTGGTCAATGGCTCTGACC  
TTGGCGTCGAGTCCAATT CGCAGTGACACCGTCCGGTGGCAGACCATCAACTCCTCCAGTACAAC  
AAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTCGTTGCATTCCAGATAACCGGCAACTC  
GGAGGAGTACATCATCGCTGAGTGGAAAGAAGACTTGA **(SEQ ID NO: 58)**

**PRIMERS FOR CONSTRUCTION OF FVE DELETION MUTANTS**

*Fd6-18F (36 mer)*

5' -ggA/TCC/TCC/gCC/ACg/TCg/TTC/gAC/TAC/ACC/CCC/AAC- 3' **(SEQ ID NO: 59)**

*Fd6-18R (36 mer)*

5' -gTT/ggg/ggT/gTA/gTC/gAA/CgA/CgT/ggC/ggA/ggA/TCC- 3' **(SEQ ID NO: 60)**

*Fd19-33F (36 mer)*

5' -TTg/gTg/AAg/AAg/ATC/gAC/ATC/gAC/AAC/CTT/ACC/TTC- 3' **(SEQ ID NO: 61)**

*Fd19-33R (36 mer)*

5' -gAA/ggT/AAg/gTT/gTC/gAT/gTC/gAT/CTT/CTT/CAC/CAA- 3' **(SEQ ID NO: 62)**

*Fd34-46F (36 mer)*

5' -ggT/ACC/CCA/AgC/AgC/TAC/AAA/TAC/TCg/TAC/CgC/gTC- 3' **(SEQ ID NO: 63)**

*Fd34-46R (36 mer)*

5' -gAC/gCg/gTA/CgA/gTA/TTT/gTA/gCT/gCT/Tgg/ggT/ACC- 3' **(SEQ ID NO: 64)**

*Fd47-60F (36 mer)*

5' -AAg/gTT/CTC/ACC/gAC/AAA/gTC/gAg/TCC/AAC/TTC/gCA- 3' **(SEQ ID NO: 65)**

*Fd47-60R (36 mer)*

5' -TgC/gAA/gTT/ggA/CTC/gAC/TTT/gTC/ggT/gAg/AAC/CTT- 3' **(SEQ ID NO: 66)**

*Fd61-72F (36 mer)*

5' -AAT/ggC/TCT/gAC/CTT/ggC/CAg/ACC/ATC/AAC/TTC/CTC- 3' **(SEQ ID NO: 67)**

*Fd61-72R (36 mer)*

5' -gAg/gAA/gTT/gAT/ggT/CTg/gCC/AAg/gTC/AgA/gCC/ATT- 3' **(SEQ ID NO: 68)**

*Fd73-84F (36 mer)*

5' -gTg/ACA/CCg/TCC/ggT/ggg/ggT/gTC/gCg/gAC/ACC/AAA- 3' **(SEQ ID NO: 69)**

*Fd73-84R (36 mer)*

5' -TTT/ggT/gTC/CgC/gAC/ACC/CCC/ACC/ggA/Cgg/TgT/CAC- 3' **(SEQ ID NO: 70)**

*Fd85-97F (36 mer)*

5' -CAg/TAC/AAC/AAg/ggg/TAT/ATT/CCA/gAT/ACC/ggC/AAC- 3' **(SEQ ID NO: 71)**

*Fd85-97R (36 mer)*

5' -gTT/gCC/ggT/ATC/Tgg/AAT/ATA/CCC/CTT/gTT/gTA/CTg- 3' (SEQ ID NO: 72)

*Fd98-106F (36 mer)*

5' -ATT/CAA/gTT/TTC/gTT/gTC/TAC/ATC/ATC/gCT/gAg/Tgg- 3' (SEQ ID NO: 73)

*Fd98-106R (36 mer)*

5' -CCA/CTC/AgC/gAT/gAT/gTA/gAC/AAC/gAA/AAC/TTg/AAT- 3' (SEQ ID NO: 74)

*Fd107-115R (39 mer)*

5' -gAT/gCA/ACT/gAA/TTC/TTA/TTA/CTC/CTC/CgA/gTT/gCC/ggT- 3' (SEQ ID NO: 75)

**PRIMERS FOR CONSTRUCTION OF LARGE FRAGMENT DELETION OF FVE**

*d(61-97)-F (36mer)*

5' -/AAT/ggC/TCT/gAC/CTT/ggC/ATT/CCA/gAT/ACC/ggC/AAC/-3' (SEQ ID NO: 76)

*d(61-97)-R (36mer)*

5' -/gTT/gCC/ggT/ATC/Tgg/AAT/gCC/AAg/gTC/AgA/gCC/ATT/-3' (SEQ ID NO: 77)

**PRIMERS FOR CONSTRUCTION OF SMALL FRAGMENT OF FVE (FROM 55AA TO 100AA)**

*[Fv55-100]-F (48mer)*

5' -  
/gTT/CCg/CgT/ggA/TCC/ATC/gAA/ggT/CgT/AAT/ggC/TCT/gAC/CTT/ggC/gTC/-3'  
(SEQ ID NO: 78)

*[Fv55-100]-R (42mer)*

5' -/gAT/gCA/ACT/gAA/TTC/TTA/TCA/ATC/Tgg/AAT/gAC/AAC/gAA/AAC/-3' (SEQ ID NO: 79)

**PRIMERS FOR CONSTRUCTION OF POINT MUTANTS OF FVE**

*F(R27A)-F (27 mer)*

5' - CCC/AAC/Tgg/ggC/gCA/ggT/ACC/CCA/AgC - 3' (SEQ ID NO: 80)

*F(R27A)-R (27 mer)*

5' - gCT/Tgg/ggT/ACC/TgC/gCC/CCA/gTT/ggg - 3' (SEQ ID NO: 81)

*F(G28A)-F (27 mer)*

5' - AAC/Tgg/ggC/CgT/gCA/ACC/CCA/AgC/AgC - 3' (SEQ ID NO: 82)

*F(G28A)-R (27 mer)*

5' - gCT/gCT/Tgg/ggT/TgC/ACg/gCC/CCA/gTT - 3' **(SEQ ID NO: 83)**

*F(T29A)-F (27 mer)*

5' - Tgg/ggC/CgT/ggT/gCA/CCA/AgC/AgC/TAC - 3' **(SEQ ID NO: 84)**

*F(T29A)-R (27 mer)*

5' - gTA/gCT/gCT/Tgg/TgC/ACC/ACg/gCC/CCA - 3' **(SEQ ID NO: 85)**

**PRIMERS FOR BLO T 5-FVE FUSION PROTEIN**

*Bt5Fv-F (36mer)*

5' - /AAg/gAT/ATT/CAA/ACC/CAA/TCC/gCC/ACg/TCg/CTC/ACC/-3' **(SEQ ID NO: 86)**

*Bt5Fv-R (36mer)*

5' - /ggT/gAg/CgA/CgT/ggC/ggA/TTg/ggT/TTg/AAT/ATC/CTT/-3' **(SEQ ID NO: 87)**

**PRIMERS FOR DER P 2-FVE FUSION PROTEIN**

*Dp2Fv-F (36mer)*

5' - /CAT/gCT/AAA/ATC/CgC/gAT/TCC/gCC/ACg/TCg/CTC/ACC-3' **(SEQ ID NO: 88)**

*Dp2Fv-R (36mer)*

5' - /ggT/gAg/CgA/CgT/ggC/ggA/ATC/gCg/gAT/TTT/AgC/ATg-3' **(SEQ ID NO: 89)**

**PRIMERS FOR BLO T 5-DER P 2-FVE FUSION PROTEIN**

*Bt5Dp2-F (36mer)*

5' - /aag/gat/att/caa/acc/caa/gat/caa/gtc/gat/gtc/aaa/-3' **(SEQ ID NO: 90)**

*Bt5Dp2-R (36mer)*

5' - /ttt/gac/atc/gac/ttg/atc/ttg/ggt/ttg/aat/atc/ctt/-3' **(SEQ ID NO: 91)**

Please delete the Appendix B header on page 172, and replace it with the following header:

**APPENDIX B: FVE FRAGMENTS (RGT TRIPLET HIGHLIGHTED)**

**(APPENDIX DISCLOSES SEQ ID NOS: 92-487, RESPECTIVELY, IN ORDER OF APPEARANCE.)**